

Amendments to the Specification:

Please replace the paragraph beginning at page 7, line 21 as with the following amended paragraph:

Figure 4. Laser scanning confocal microscopy (LSCM) demonstrates that the characteristic cytokeratin staining pattern of the tissue biopsies (left panels of Figure 4) has been retained in the respective primary cervical epithelial cell cultures (right panels of Figure 4). Sectioned tissue biopsies and primary cervical epithelial cell monolayers were incubated with a FITC-conjugated antibody to the noted specific cytokeratin. Ethidium bromide was used to counter-stain the tissue sections. Endocervical cells labeled intensely with antibody 8.12, which is specific for type I cytokeratins 13, 15, and 16 (panel A1 and A2). The labeling of endocervical cells with an antibody specific for type II cytokeratin 4 (panel C1 and C2) was considerably less intense, and it was not uniformly distributed. Ectocervical cells labeled positive with an antibody specific for cytokeratins 13, 15, and 16 (panel B1 and B2) and cytokeratin 4 (panel D1 and D2).

Please replace the paragraph beginning at page 22, line 5 as with the following amended paragraph:

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T. is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased.

Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always>0) and N (penalty score for mismatching residues; always<0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

Please replace the paragraph beginning at page 81, line 12 as with the following amended paragraph:

Individual, smaller peptides based on the sequence of rI-domain duplicate the inhibitory activity of the rI-domain. ~~[fill in once studies completed]~~